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## RAW SEQUENCE LISTING

DATE: 03/18/2002

PATENT APPLICATION: US/09/809,920

TIME: 16:04:58

Input Set : N:\Crf3\RULE60\09809920.raw

Output Set: N:\CRF3\03182002\I809920.raw

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Sato, Takaaki

7 (ii) TITLE OF INVENTION: TREX, A NOVEL GENE OF TRAF-INTERACTING

8 EXT GENE FAMILY AND DIAGNOSTIC AND THERAPEUTIC USES  
9 THEREOF

11 (iii) NUMBER OF SEQUENCES: 37

13 (iv) CORRESPONDENCE ADDRESS:

14 (A) ADDRESSEE: Cooper &amp; Dunham LLP

15 (B) STREET: 1185 Avenue of the Americas

16 (C) CITY: New York

17 (D) STATE: New York

18 (E) COUNTRY: U.S.A

19 (F) ZIP: 10036

21 (v) COMPUTER READABLE FORM:

22 (A) MEDIUM TYPE: Floppy disk

23 (B) COMPUTER: IBM PC compatible

24 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

25 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

27 (vi) CURRENT APPLICATION DATA:

C--&gt; 28 (A) APPLICATION NUMBER: US/09/809,920

C--&gt; 29 (B) FILING DATE: 16-Mar-2001

30 (C) CLASSIFICATION:

32 (vii) PRIOR APPLICATION DATA:

33 (A) APPLICATION NUMBER: US/09/156,191

34 (B) FILING DATE:

37 (viii) ATTORNEY/AGENT INFORMATION:

38 (A) NAME: White, John P.

39 (B) REGISTRATION NUMBER: 28,678

40 (C) REFERENCE/DOCKET NUMBER: 0575/51902

42 (ix) TELECOMMUNICATION INFORMATION:

43 (A) TELEPHONE: (212) 278-0400

44 (B) TELEFAX: (212) 391-0525

47 (2) INFORMATION FOR SEQ ID NO: 1:

49 (i) SEQUENCE CHARACTERISTICS:

50 (A) LENGTH: 3479 base pairs

51 (B) TYPE: nucleic acid

52 (C) STRANDEDNESS: single

53 (D) TOPOLOGY: linear

55 (ii) MOLECULE TYPE: DNA (genomic)

58 (ix) FEATURE:

59 (A) NAME/KEY: CDS

60 (B) LOCATION: 458..3211

ENTERED

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63      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
64      CCTGATCGTT GGTAGTGGCA TGGAGGACGG GGCTGGCATT TCAGACTGCC AGCTGTTTTT      60
65      ACCAGCCGCT GCATCACTTG AATAGAAGCT ATGCATATTG GCTGGCCGAC AAAGCCAAGG      120
66      GACAAAAGCT ATGGCCGTTA AAATGGTCCC TCTGAGTCCA GGGCTCTTTC CCTGGCTTTT      180
67      AGCACCATGG ATCTCTTCCT TTTCATCCCA TCAGCAATGT GGTACCTTCT TCTACTTGAT      240
68      GATGACAGCT GATACTTCAG ATTTGCCTGA CTAAGGTTAG AAACCTGAAT CGCTGTGAGG      300
69      AAGATGAAAT TTCCATTTTA CTTGGTGCCT TGTGCAGGGA GCACACTGAT CCTTCCAGAA      360
70      ACTTGTGTGT GAAAAGAGGT TGCCTTTTGT CAGACAGACT CATGGTTATG GCGAGCGATC      420
71      CGACGTGATC AGAGTGGGCA AGAGGCACAG CGAACTC ATG ACA GGC TAT ACC ATG      475
72      Met Thr Gly Tyr Thr Met
73      1 5
74      TTG CGG AAT GGG GGA GTG GGG AAC GGT GGT CAG ACC TGT ATG CTG CGC      523
75      Leu Arg Asn Gly Gly Val Gly Asn Gly Gly Gln Thr Cys Met Leu Arg
76      10 15 20
77      TGG TCC AAT CGC ATC CGG CTG ACA TGG CTG AGT TTC ACG CTG TTC ATC      571
78      Trp Ser Asn Arg Ile Arg Leu Thr Trp Leu Ser Phe Thr Leu Phe Ile
79      25 30 35
80      ATC CTC GTC TTC TTC CCC CTC ATT GCT CAC TAT TAC CTC ACC ACT CTG      619
81      Ile Leu Val Phe Phe Pro Leu Ile Ala His Tyr Tyr Leu Thr Thr Leu
82      40 45 50
83      GAC GAG GCA GAC GAG GCT GGC AAG CGC ATC TTC GGC CCT CGG GCT GGC      667
84      Asp Glu Ala Asp Glu Ala Gly Lys Arg Ile Phe Gly Pro Arg Ala Gly
85      55 60 65 70
86      AGT GAG CTC TGT GAG GTA AAG CAT GTC CTT GAT CTC TGT CGG ATT CGT      715
87      Ser Glu Leu Cys Glu Val Lys His Val Leu Asp Leu Cys Arg Ile Arg
88      75 80 85
89      GAG TCT GTG AGC GAA GAG CTT CTA CAG CTC GAA GCC AAG CGG CAG GAG      763
90      Glu Ser Val Ser Glu Glu Leu Leu Gln Leu Glu Ala Lys Arg Gln Glu
91      90 95 100
92      CTG AAC AGC GAG ATT GCC AAG CTG AAC CTC AAG ATT GAA GCC TGT AAG      811
93      Leu Asn Ser Glu Ile Ala Lys Leu Asn Leu Lys Ile Glu Ala Cys Lys
94      105 110 115
95      AAG AGC ATA GAG AAT GCC AAG CAG GAC CTG CTG CAG CTC AAG AAT GTC      859
96      Lys Ser Ile Glu Asn Ala Lys Gln Asp Leu Leu Gln Leu Lys Asn Val
97      120 125 130
98      ATT AGC CAG ACA GAG CAC TCC TAC AAG GAG CTG ATG GCC CAG AAC CAG      907
99      Ile Ser Gln Thr Glu His Ser Tyr Lys Glu Leu Met Ala Gln Asn Gln
100      135 140 145 150
101      CCC AAA CTG TCC CTG CCC ATC CGA CTG CTC CCT GAG AAG GAC GAT GCC      955
102      Pro Lys Leu Ser Leu Pro Ile Arg Leu Leu Pro Glu Lys Asp Asp Ala
103      155 160 165
104      GGC CTT CCA CCC CCC AAG GTC ACT CGG GGT TGC CGC CTT CAC AAC TGC      1003
105      Gly Leu Pro Pro Pro Lys Val Thr Arg Gly Cys Arg Leu His Asn Cys
106      170 175 180
107      TTT GAT TAC TCT CGT TGT CCT CTG ACG TCT GGC TTT CCC GTC TAC GTC      1051
108      Phe Asp Tyr Ser Arg Cys Pro Leu Thr Ser Gly Phe Pro Val Tyr Val
109      185 190 195
110      TAT GAC AGT GAC CAG TTT GCC TTT GGG AGC TAC CTG GAC CCT TTG GTC      1099
111      Tyr Asp Ser Asp Gln Phe Ala Phe Gly Ser Tyr Leu Asp Pro Leu Val

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Input Set : N:\Crif3\RULE60\09809920.raw

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133	200	205	210	
135	AAG CAG GCT TTT CAG GCT ACA GTG AGA GCC AAC GTT TAT GTT ACA GAA	1147		
136	Lys Gln Ala Phe Gln Ala Thr Val Arg Ala Asn Val Tyr Val Thr Glu			
137	215 220 225 230			
139	AAT GCG GCC ATC GCC TGC CTG TAT GTG GTG TTA GTG GGA GAA ATG CAA	1195		
140	Asn Ala Ala Ile Ala Cys Leu Tyr Val Val Leu Val Gly Glu Met Gln			
141	235 240 245			
143	GAG CCC ACT GTG CTG CGG CCT GCC GAC CTT GAA AAG CAG CTG TTT TCT	1243		
144	Glu Pro Thr Val Leu Arg Pro Ala Asp Leu Glu Lys Gln Leu Phe Ser			
145	250 255 260			
147	CTG CCA CAC TGG AGG ACA GAT GGG CAC AAC CAC GTC ATT ATC AAC CTG	1291		
148	Leu Pro His Trp Arg Thr Asp Gly His Asn His Val Ile Ile Asn Leu			
149	265 270 275			
151	TCC CGG AAG TCA GAC ACA CAG AAT CTA CTG TAC AAC GTC AGT ACA GGC	1339		
152	Ser Arg Lys Ser Asp Thr Gln Asn Leu Leu Tyr Asn Val Ser Thr Gly			
153	280 285 290			
155	CGC CAT GTG GCC CAG TCC ACC CTC TAT GCT GCC CAG TAC AGA GCT GGC	1387		
156	Arg His Val Ala Gln Ser Thr Leu Tyr Ala Ala Gln Tyr Arg Ala Gly			
157	295 300 305 310			
159	TTT GAC CTG GTC GTG TCA CCC CTT GTC CAT GCT ATG TCT GAA CCC AAC	1435		
160	Phe Asp Leu Val Val Ser Pro Leu Val His Ala Met Ser Glu Pro Asn			
161	315 320 325			
163	TTC ATG GAA ATC CCA CCG CAG GTG CCA GTT AAG CGG AAA TAT CTC TTC	1483		
164	Phe Met Glu Ile Pro Pro Gln Val Pro Val Lys Arg Lys Tyr Leu Phe			
165	330 335 340			
167	ACT TTC CAG GGC GAG AAG ATC GAG TCT CTG AGA TCT AGC CTT CAG GAG	1531		
168	Thr Phe Gln Gly Glu Lys Ile Glu Ser Leu Arg Ser Ser Leu Gln Glu			
169	345 350 355			
171	GCC CGT TCC TTC GAG GAA GAG ATG GAG GGC GAC CCT CCG GCC GAC TAT	1579		
172	Ala Arg Ser Phe Glu Glu Glu Met Glu Gly Asp Pro Pro Ala Asp Tyr			
173	360 365 370			
175	GAC GAT CGC ATC ATT GCC ACC CTA AAG GCT GTA CAG GAC AGC AAG CTG	1627		
176	Asp Asp Arg Ile Ile Ala Thr Leu Lys Ala Val Gln Asp Ser Lys Leu			
177	375 380 385 390			
179	GAT CAG GTG CTG GTA GAA TTC ACT TGC AAA AAC CAG CCG AAG CCT AGC	1675		
180	Asp Gln Val Leu Val Glu Phe Thr Cys Lys Asn Gln Pro Lys Pro Ser			
181	395 400 405			
183	CTG CCG ACT GAG TGG GCA CTG TGT GGG GAG CGG GAA GAC CGC CTG GAG	1723		
184	Leu Pro Thr Glu Trp Ala Leu Cys Gly Glu Arg Glu Asp Arg Leu Glu			
185	410 415 420			
187	TTA CTG AAG CTC TCC ACC TTC GCC CTC ATC ATC ACT CCC GGG GAC CCG	1771		
188	Leu Leu Lys Leu Ser Thr Phe Ala Leu Ile Ile Thr Pro Gly Asp Pro			
189	425 430 435			
191	CGC CTG CTC ATT TCA TCT GGG TGT GCC ACG CGG CTC TTC GAG GCC CTG	1819		
192	Arg Leu Leu Ile Ser Ser Gly Cys Ala Thr Arg Leu Phe Glu Ala Leu			
193	440 445 450			
195	GAG GTG GGG GCC GTG CCG GTG GTG CTC GGG GAG CAG GTG CAG CTC CCG	1867		
196	Glu Val Gly Ala Val Pro Val Val Leu Gly Glu Gln Val Gln Leu Pro			
197	455 460 465 470			

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199	TAC	CAC	GAC	ATG	CTG	CAG	TGG	AAC	GAG	GCC	GCC	CTG	GTG	GTG	CCC	AAG	1915
200	Tyr	His	Asp	Met	Leu	Gln	Trp	Asn	Glu	Ala	Ala	Leu	Val	Val	Pro	Lys	
201					475					480						485	
203	CCT	CGC	GTC	ACA	GAG	GTC	CAC	TTC	CTG	TTA	CGA	AGT	CTT	TCA	GAC	AGT	1963
204	Pro	Arg	Val	Thr	Glu	Val	His	Phe	Leu	Leu	Arg	Ser	Leu	Ser	Asp	Ser	
205					490					495						500	
207	GAT	CTG	TTG	GCC	ATG	AGG	CGG	CAA	GGC	CGC	TTT	CTC	TGG	GAG	ACC	TAC	2011
208	Asp	Leu	Leu	Ala	Met	Arg	Arg	Gln	Gly	Arg	Phe	Leu	Trp	Glu	Thr	Tyr	
209					505					510						515	
211	TTC	TCC	ACC	GCA	GAC	AGT	ATT	TTT	AAT	ACC	GTG	CTG	GCC	ATG	ATT	AGG	2059
212	Phe	Ser	Thr	Ala	Asp	Ser	Ile	Phe	Asn	Thr	Val	Leu	Ala	Met	Ile	Arg	
213					520					525						530	
215	ACT	CGA	ATT	CAG	ATC	CCA	GCT	GCT	CCC	ATC	CGG	GAA	GAG	GTA	GCG	GCT	2107
216	Thr	Arg	Ile	Gln	Ile	Pro	Ala	Ala	Pro	Ile	Arg	Glu	Glu	Val	Ala	Ala	
217	535									540						550	
219	GAG	ATC	CCC	CAT	CGT	TCA	GGC	AAA	GCA	GCT	GGA	ACT	GAC	CCC	AAC	ATG	2155
220	Glu	Ile	Pro	His	Arg	Ser	Gly	Lys	Ala	Ala	Gly	Thr	Asp	Pro	Asn	Met	
221					555						560					565	
223	GCT	GAC	AAT	GGG	GAC	CTG	GAC	CTG	GGG	CCG	GTA	GAG	ACA	GAA	CCA	CCC	2203
224	Ala	Asp	Asn	Gly	Asp	Leu	Asp	Leu	Gly	Pro	Val	Glu	Thr	Glu	Pro	Pro	
225					570					575						580	
227	TAT	GCC	TCA	CCT	AAA	TAC	CTC	CGC	AAT	TTC	ACT	CTG	ACT	GTC	ACA	GAC	2251
228	Tyr	Ala	Ser	Pro	Lys	Tyr	Leu	Arg	Asn	Phe	Thr	Leu	Thr	Val	Thr	Asp	
229					585					590						595	
231	TGT	TAC	CGT	GGC	TGG	AAC	TCT	GCC	CCG	GGA	CGG	TTC	CAT	CTT	TTT	CCC	2299
232	Cys	Tyr	Arg	Gly	Trp	Asn	Ser	Ala	Pro	Gly	Arg	Phe	His	Leu	Phe	Pro	
233					600					605						610	
235	CAC	ACA	CCC	TTT	GAT	CCT	GTG	TTG	CCC	TCT	GAG	GCC	AAA	TTC	TTG	GGC	2347
236	His	Thr	Pro	Phe	Asp	Pro	Val	Leu	Pro	Ser	Glu	Ala	Lys	Phe	Leu	Gly	
237	615									620						630	
239	TCA	GGG	ACT	GGA	TTT	CGG	CCG	ATC	GGT	GGC	GGG	GCT	GGG	GGC	TCT	GGC	2395
240	Ser	Gly	Thr	Gly	Phe	Arg	Pro	Ile	Gly	Gly	Gly	Ala	Gly	Gly	Ser	Gly	
241					635						640					645	
243	AAG	GAG	TTC	CAG	GCA	GCG	CTC	GGA	GGC	AAT	GTC	CAG	CGG	GAG	CAG	TTC	2443
244	Lys	Glu	Phe	Gln	Ala	Ala	Leu	Gly	Gly	Asn	Val	Gln	Arg	Glu	Gln	Phe	
245					650					655						660	
247	ACA	GTT	GTG	ATG	CTG	ACC	TAC	GAG	CGG	GAG	GAA	GTG	CTC	ATG	AAC	TCC	2491
248	Thr	Val	Val	Met	Leu	Thr	Tyr	Glu	Arg	Glu	Glu	Val	Leu	Met	Asn	Ser	
249					665					670						675	
251	CTG	GAG	AGA	CTC	AAC	GGC	CTC	CCC	TAC	CTG	AAC	AAG	GTA	GTG	GTG	GTG	2539
252	Leu	Glu	Arg	Leu	Asn	Gly	Leu	Pro	Tyr	Leu	Asn	Lys	Val	Val	Val	Val	
253					680					685						690	
255	TGG	AAC	TCT	CCC	AAG	CTG	CCC	TCG	GAG	GAC	CTT	TTG	TGG	CCA	GAC	ATT	2587
256	Trp	Asn	Ser	Pro	Lys	Leu	Pro	Ser	Glu	Asp	Leu	Leu	Trp	Pro	Asp	Ile	
257	695									700						710	
259	GGT	GTC	CCC	ATC	ATG	GTC	GTC	CGT	ACT	GAG	AAG	AAC	AGT	TTG	AAC	AAT	2635
260	Gly	Val	Pro	Ile	Met	Val	Val	Arg	Thr	Glu	Lys	Asn	Ser	Leu	Asn	Asn	
261					715						720					725	
263	CGG	TTC	TTG	CCC	TGG	AAT	GAG	ATT	GAG	ACA	GAG	GCC	ATA	CTG	TCC	ATC	2683

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264 Arg Phe Leu Pro Trp Asn Glu Ile Glu Thr Glu Ala Ile Leu Ser Ile
265          730          735          740
267 GAC GAT GAT GCT CAC CTC CGC CAT GAT GAA ATC ATG TTT GGG TTT TGG      2731
268 Asp Asp Asp Ala His Leu Arg His Asp Glu Ile Met Phe Gly Phe Trp
269          745          750          755
271 GTG TGG AGA GAA GCA CGT GAT CGC ATT GTG GGT TTC CCT GGC CGG TAC      2779
272 Val Trp Arg Glu Ala Arg Asp Arg Ile Val Gly Phe Pro Gly Arg Tyr
273          760          765          770
275 CAT GCG TGG GAC ATC CCG CAC CAG TCC TGG CTC TAC AAT TCC AAC TAC      2827
276 His Ala Trp Asp Ile Pro His Gln Ser Trp Leu Tyr Asn Ser Asn Tyr
277 775          780          785          790
279 TCC TGT GAG CTG TCC ATG GTG CTG ACG GGC GCT GCC TTC TTT CAC AAG      2875
280 Ser Cys Glu Leu Ser Met Val Leu Thr Gly Ala Ala Phe Phe His Lys
281          795          800          805
283 TAT TAT GCC TAC CTG TAT TCT TAT GTG ATG CCC CAG GCC ATC CGG GAC      2923
284 Tyr Tyr Ala Tyr Leu Tyr Ser Tyr Val Met Pro Gln Ala Ile Arg Asp
285          810          815          820
287 ATG GTG GAC GAG TAC ATC AAC TGT GAG GAT ATC GCC ATG AAC TTC CTT      2971
288 Met Val Asp Glu Tyr Ile Asn Cys Glu Asp Ile Ala Met Asn Phe Leu
289          825          830          835
291 GTC TCC CAC ATC ACA CGG AAA CCC CCC ATC AAG GTG ACA TCA AGG TGG      3019
292 Val Ser His Ile Thr Arg Lys Pro Pro Ile Lys Val Thr Ser Arg Trp
293          840          845          850
295 ACT TTT CGA TGC CCA GGG TGC CCT CAG GCC CTG TCC CAT GAT GAC TCT      3067
296 Thr Phe Arg Cys Pro Gly Cys Pro Gln Ala Leu Ser His Asp Asp Ser
297 855          860          865          870
299 CAT TTT CAC GAG CGG CAC AAG TGT ATC AAC TTT TTT GTC AAG GTG TAC      3115
300 His Phe His Glu Arg His Lys Cys Ile Asn Phe Phe Val Lys Val Tyr
301          875          880          885
303 GGC TAT ATG CCT CTC TTG TAC ACA CAG TTC AGG GTG GAC TCC GTG CTC      3163
304 Gly Tyr Met Pro Leu Leu Tyr Thr Gln Phe Arg Val Asp Ser Val Leu
305          890          895          900
307 TTC AAG ACC CGC CTG CCC CAT GAC AAG ACC AAG TGC TTC AAG TTC ATC      3211
308 Phe Lys Thr Arg Leu Pro His Asp Lys Thr Lys Cys Phe Lys Phe Ile
309          905          910          915
311 TAGGGCCTTG CAGTTCTGAG GAGACAATGA GCAGAGCGAG GGGGAGTCAC CCTCAAGGTT      3271
313 CCCAAGGTGT CGAAGGTCCT TGGGGACATC TGTCGGGCAG GGCCAAGACC CTTTGCTGGG      3331
315 AGAGGCAGCA GGAAGAGTGG AAAGGGATAG CTGTCTTTCA TTTTGAAGTC AGCCACACTG      3391
317 GGCCTGGGAT CCTGGTCAGA GACTCAGGNC GTCTGCACAG GGCCTGACT GATAGCGAAC      3451
319 ACTGAGGACT GTTCATAAGC CCAGGACA      3479
322 (2) INFORMATION FOR SEQ ID NO: 2:
324     (i) SEQUENCE CHARACTERISTICS:
325         (A) LENGTH: 918 amino acids
326         (B) TYPE: amino acid
327         (D) TOPOLOGY: linear
329     (ii) MOLECULE TYPE: protein
331     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
333 Met Thr Gly Tyr Thr Met Leu Arg Asn Gly Gly Val Gly Asn Gly Gly
334   1              5              10              15

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Input Set : N:\Crf3\RULE60\09809920.raw

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L:28 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:29 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:549 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:553 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:557 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:561 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:565 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:569 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:573 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:577 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:581 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:585 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:589 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:593 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:597 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
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L:673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
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L:685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:693 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
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L:725 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:729 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3

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L:733 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:737 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:741 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3  
L:745 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3